行政院國家科學委員會專題研究計畫　成果報告

海洋環境對珊瑚族群散布及群聚結構的影響

計畫類別：個別型計畫
計畫編號：NSC93-2611-M-002-004-
執行期間：93 年 08 月 01 日至 94 年 07 月 31 日
執行單位：國立臺灣大學海洋研究所

計畫主持人：戴昌鳳

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報告類型：精簡報告

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執行單位：台灣大學海洋研究所

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一、研究成果概述

1. 台灣海域三種雀鯛的族群相連性與海流的關係

台灣沿岸的海洋環境主要受到黑潮、南中國海表層流與中國沿岸流的影響，而且此三大水團具有明顯的季節變動，這種變動可能會影響海洋生物的散佈和族群分化。而珊瑚礁魚類的幼生隨海流而散佈，其散佈距離則與浮游期的長短有關。本研究選擇三種廣泛分布，並具有不同幼生漂浮期的雀鯛科魚類(克氏海葵魚、變色雀鯛、太平洋真雀鯛)為材料，使用高變異性的微隨體DNA為分子標誌，探討幼生浮游期與季節性海流變動對魚類族群結構和相連性的影響。目前初步針對克氏海葵魚與變色雀鯛進行微隨體基因座的篩選與多型性的判讀，前者共獲得五組具多型性的基因座，其中兩組基因座從1700個轉殖菌株中篩選出且未發表，後者則有六組具多型性的基因座，其中三組從2500個轉殖菌株中篩出且未發表，其餘為發表過的基因座。變色雀鯛六組基因座的異型合子觀測值介於0.437-0.875 (n=171)，異型合子歧異度期望值介於0.556-0.897；克氏海葵魚五組基因座的異型合子觀測值介於0.295-0.785 (n=73)，異型合子期望值介於0.455-0.965。結果顯示這些基因座可應用於族群結構與地理親緣分析的基礎。

The coastal waters around Taiwan are characterized by a wide array of environments encompassing tropics to subtropics and under the influences of seasonal variations of water masses from the Kuroshio, the South China Sea and the East China Sea. The seasonal variations of current patterns around Taiwan may have significant influences on marine populations. Previous studies have indicated that the genetic structure of coral populations is related to current patterns. However, the interplays between hydrographic conditions and life history feature (duration time) of damselfishes and its influences on population structures remain to be studied. In this study, we focus on three species of Pomacentridae (i.e., *Amphiprion clarkii*, *Pomacentrus coelestis* and *Stegastes faciolatus*) with different pelagic durations. We used polymorphic microsatellite loci to reveal the genetic connectivity between populations around Taiwan. We have screened the polymorphic loci and tested their level of polymorphism. In *P. coelestis*, 6 polymorphic loci were found and 3 were screened from 2500 colonies and unpublished. In *A. clarkii*, 5 polymorphic loci were obtained and 2 were screened from 1700 colonies and unpublished. The observed heterozygosity of *P. coelestic* among 6 loci ranged from 0.437 to 0.875 (n=171) and the expected heterozygosity ranged from 0.556 to 0.897. The observed heterozygosity of *A. clarkii* among 5 loci range from 0.295 to 0.785 (n=73) and the expected heterozygosity ranged from 0.455 to 0.965. The preliminary results suggest that these loci have sufficient genetic variations that can be applied to further analyses of population structure and phylogeographic relationships.

2. Species delineation and cryptic status of *Seriatopora* (台灣海域列孔珊瑚屬的種間界限)

Seriatopora species are characterized by their corallites arranging in neat rows along the branches. They are known for wide variations of their corallum and colony morphologies. Previous studies assumed that *Seriatopora* species contained a certain degree of phenotypic plasticity, especially those from different environments. Three major species groups or six species have been recognized according to their differences in colony morphology and branch diameter, respectively. However, phenotypic plasticity and species boundaries of *Seriatopora* corals remain to be studied. In this study, the phylogeny of a mitochondrial intergenic region was used to interpret the species boundaries of *Seriatopora*. The *S. caliendrum* group, two species of *S. hystrix* group (*S. hystrix, S. dendritica*) and *S. stellata* group (*S. stellata*, *S. gutatus*) were used as the sampling units. Samples were collected from several reefs of Taiwan, South China Sea and Andaman Sea. The mitochondria genome of S. caliendrum is 17,006 bp containing 13 protein coding genes, 2 rRNA genes, and 3 tRNA genes (1 $tRNA^{Met}$, 2 $tRNA^{Cys}$) (Table 1). Its genome structure is similar to that of *Acropora tenuis* (Fig. 1). There were three phylogenic clades with significant genetic differentiation, but no concordances with previous taxonomic and geographic groupings (Fig. 2). *S. caliendrum* from shallow water of Taiping Island in the Sprathys formed a monophyletic group. *S. hystrix* clade includes *S. hystrix* and *S. dendritica* samples of the three regions. *S. caliendrum* and *S. stellata* form Taiwan and *S. caliendrum* from deep water of Taiping Island form a paraphyletic group. These results indicate the possibility of cryptic species of *Seriatopora*.

3. 台灣海域紅鞭珊瑚(*Junceella juncea*)的遺傳結構分析

我們以兩種方法(1)傳統南方轉漬法，搜尋非完整基因庫中具有微衛星體 DNA 的片段(partial library screen), (2)增幅選殖法(enrichment screen)篩選紅鞭珊瑚(*Junceella juncea*)的微衛星體 DNA。由選殖結果發現紅鞭珊瑚基因組內微衛星體 DNA 可能很少，其中能成功以 PCR 增幅及具有多型性的基因座共有 4 組。以此 4 組基因座探討台灣北部石城、南部下水堀與南灣海域三個地理族群的基因體結構，結果顯示 4 組有變異的微隨體基因座可將 152 個群體劃分成 40 個基因型，基因型歧異度(genotypic diversity)觀測值(G_o)與理想值(G_e)的比值範圍為 0.018 到 0.422，由此可知紅鞭珊瑚地區性族群主要是由無性生殖所貢獻，而有性生殖的添入則扮演族群的奠基者(founder)。

4. 澎湖海域的珊瑚群聚型態

針對澎湖北海、南海、東海及內海海域，於各海域選定三個離島或地點，作為本研究之初步調查地點，每個地點相距 7-10 公里，每個地點兩個不同的深度，隨機選取六條「橫截線」(transect lines) 當作樣本，各線之間相距約 10 公尺。以此空間尺度的巢式取樣設計，瞭解不同尺度的群聚變異。所得結果以 PRIMER 5.0 進行資料分析。初步分析結果顯示，(1)在 12 個地點中，瓦硐是一個外離群；(2)內海形成一群；(3)北海及東海形成另一群；(4)南海區域則是七美及嶼坪形成一群，大塭則是跟東海、北海類群較接近。若是以多向尺度分析(MDS)結果則發現：(1)選定的 12 個地點當中，瓦硐仍然是一個外離群；(2)內海形成一群（除了瓦硐之外）；(3)北海及東海則形成一群；(4)南海區域則是一群(Fig. 3)。上述初步結果顯示澎湖海域的珊瑚群聚型態特殊，將進一步做更詳細的採樣研究及探究其形成機制。

二、成果發表

1. Liu SV, Dai CF, Yu HT (2005) Cloning and characterization of microsatellite loci in a gorgonian coral, *Junceella juncea* (Anthozoa; Octocorallia; Ellisellidae) and its application in clonal genotyping. Marine Biotechnology 7: 26-32.
2. Liu SV, Yu HT, Dai CF (2005) Genotyping the clonal structure of a gorgonian coral, *Junceella juncea* (Anthozoa: Octocorallia), using microsatellite loci. Coral Reefs (in press)
3. Liu SV, Yu HT, Dai CF (2005) The genetic connectivity of damselfish around Taiwan: a preliminary study. Workshop on Molecular Phylogeny of Scleractinian Corals and Reef Connectivity of the South and East China Sea Boards. Academia Sinica, Taipei.
4. Chen CS, Chen CA, Dai CF (2005)Species delineation and cryptic status of *Seriatopora*. Workshop on Molecular Phylogeny of Scleractinian Corals and Reef Connectivity of the South and East China Sea Boards. Academia Sinica, Taipei.

Table 1. Positions and sizes of all coding and non-coding regions and initiation/ termination codons of all protein-coding genes of the S. caliendrum mitochondrial genome.

Position	Region	Start codon	Stop codon	Length (bp)
1-71	tRNA-M			71
72-1973	Lr RNA (?)			1902
1974-2684	ND5 5’	ATG		711
2685-2782	IGR1			98
2783-3787	ND1	ATT	TAA	1005
3788-3806	IGR2			19
3807-4961	COB	GTG	TAG	1155
4962-5165	IGR3			204
5166-6254	ND2	ATT	TAA	1089
6255-6256	IGR4			2
6257-6820	ND6	ATG	TAA	564
6820-7497	ATP6	ATG	TAA	678
7498-8476	Putative CR			979
8477-9937	ND4	GTG	TAG	1461
9938-9948	IGR5			11
9949-10866	Sr RNA			918
10864-11646	COIII	TTG	TAA	783
11647-11698	IGR6			52
11699-12439	COII	ATG	TAG	741
12422-12718	ND4L	ATG	TAA	297
12719-13063	ND3	ATG	TAA	345
13064-13117	IGR7			54
13118-14326	ND5 3’		TAG	1209
14256-14325	tRNA-C			70
14327-14356	IGR8			31
14357-14596	ATP8	ATA	TAG	240
14597-14690	IGR9			94
14691-14760	tRNA-C			70
14761-15413	IGR10			653
15414-17006	COI	ATA	TAA	1593

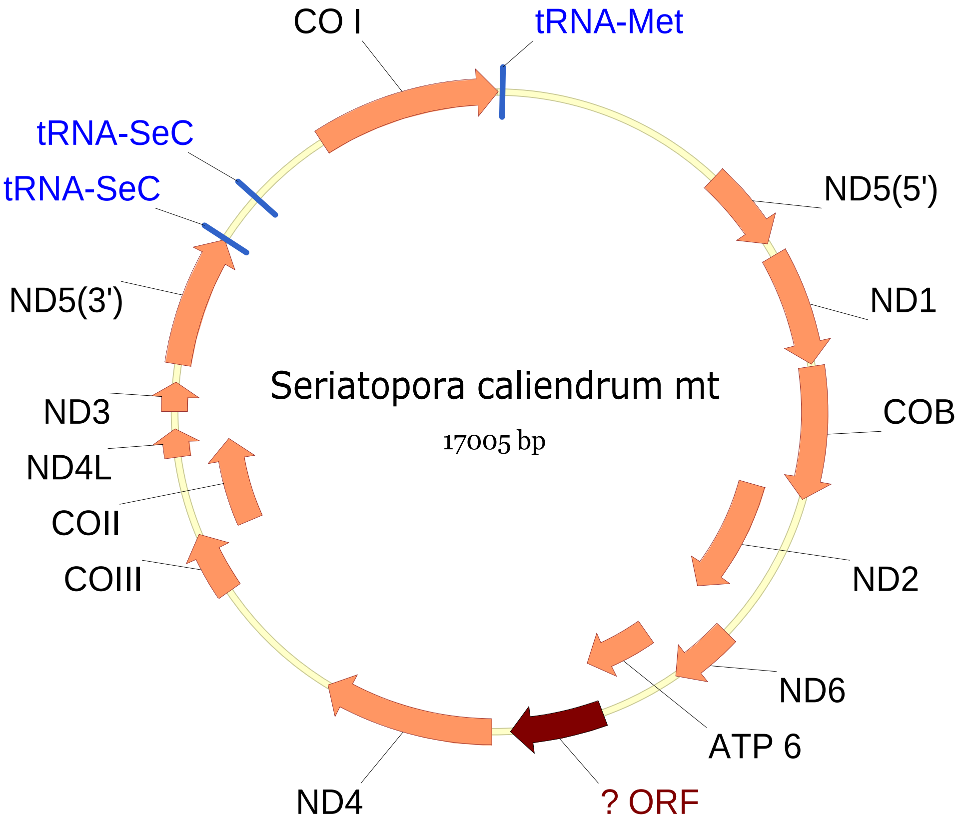

Fig. 1. Schematic overview of the gene map of complete *Seriatopora caliendrum* mitochondrial DNA. Numbers below the figure represent the sizes of the intergenetic regions. The tRNAs are black and the arrow indicates the direction of transcription.

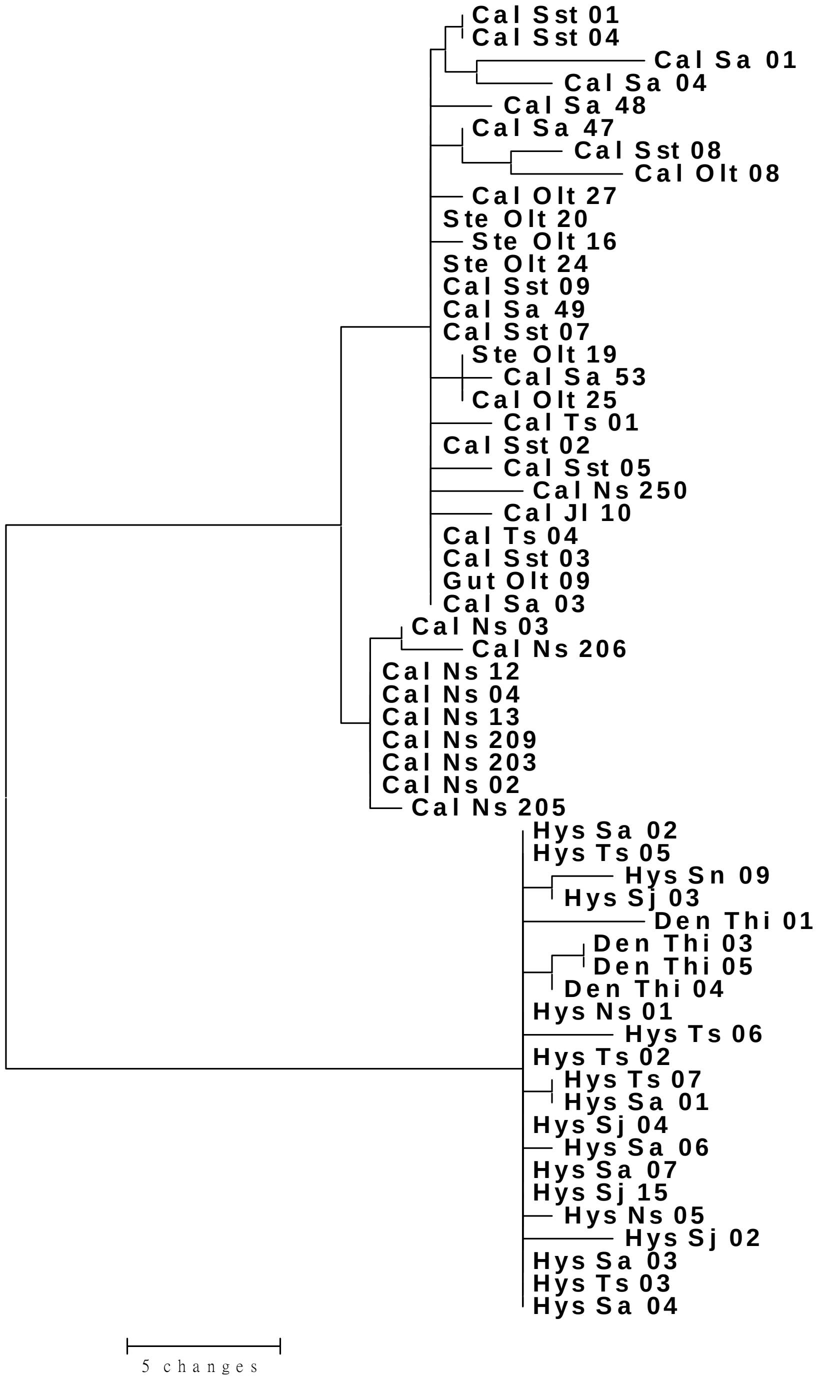

Fig. 2. Phylogenetic analysis of *Seriatopora* species showing three clades.

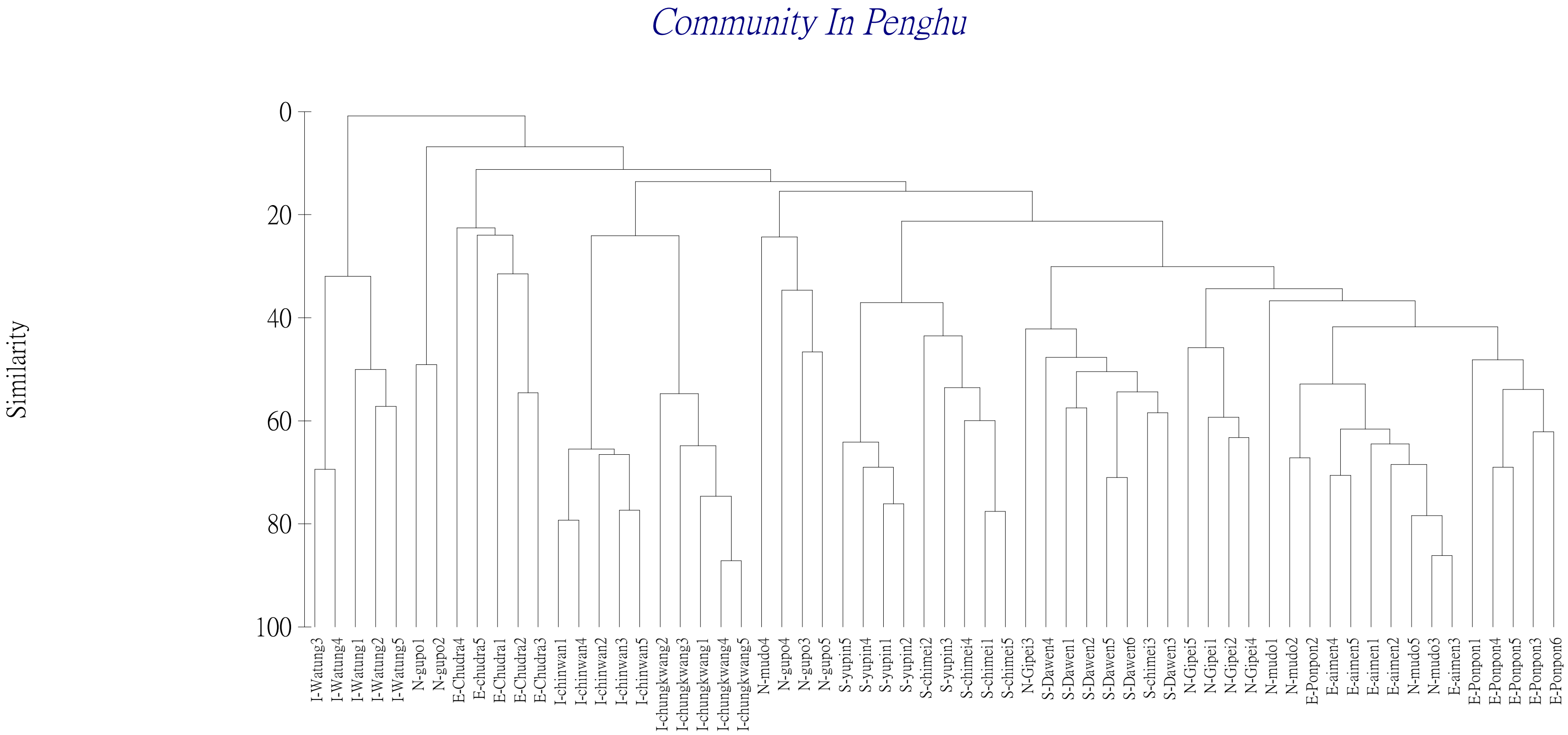

Fig. 3. Cluster analysis of coral communities in Penghu Islands.